





GenCore version 4.5  
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ON nucleic - nucleic search, using SW model

Run on: March 24, 2000, 10:59:29 ; Search time 3493.2 Seconds  
(without alignments)  
669.053 Million cell updates/sec

Title: US-09-276-268-3  
Perfect score: 619  
Sequence: 1 ggcacaggaagccctgc.....tggtgccaagcccaactta 619  
Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4538634 seqs, 188731982 residues

Total number of hits satisfying chosen parameters: 907768

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database :

28: em\_est1.\*

2: em\_est2.\*

3: em\_est3.\*

4: em\_est4.\*

5: em\_est5.\*

6: em\_est6.\*

7: em\_est7.\*

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42: em\_est42.\*

43: em\_est43.\*

44: em\_est44.\*

45: em\_est45.\*

45: gb\_est26.\*  
46: gb\_est27.\*  
47: gb\_est28.\*  
48: gb\_est29.\*  
49: gb\_est30.\*  
50: gb\_est31.\*  
51: gb\_est32.\*  
52: gb\_est33.\*  
53: gb\_est34.\*  
54: em\_est22.\*  
55: em\_est21.\*  
56: em\_est20.\*  
57: em\_est19.\*  
58: em\_est18.\*  
59: gb\_est35.\*  
60: gb\_est36.\*  
61: gb\_est37.\*  
62: gb\_est38.\*  
63: gb\_est39.\*  
64: gb\_est40.\*  
65: em\_est27.\*  
66: em\_est26.\*  
67: em\_est25.\*  
68: em\_est24.\*  
69: gb\_est39.\*  
70: gb\_est40.\*  
71: gb\_est41.\*  
72: gb\_est42.\*  
73: gb\_est43.\*  
74: gb\_est44.\*  
75: gb\_est45.\*  
76: em\_est32.\*  
77: em\_est33.\*  
78: em\_est34.\*  
79: em\_est35.\*  
80: gb\_est46.\*  
81: gb\_est47.\*  
82: gb\_est48.\*  
83: em\_est36.\*  
84: em\_est37.\*  
85: em\_est38.\*  
86: em\_est39.\*  
87: gb\_est49.\*  
88: gb\_est50.\*  
89: gb\_est51.\*  
90: gb\_est52.\*  
91: gb\_est53.\*  
92: em\_est35.\*  
93: em\_est36.\*  
94: em\_est37.\*  
95: em\_est38.\*  
96: em\_est39.\*  
97: em\_est40.\*  
98: gb\_est54.\*  
99: gb\_est55.\*  
100: gb\_est56.\*  
101: em\_est41.\*  
102: em\_est42.\*  
103: gb\_est57.\*  
104: gb\_est58.\*  
105: gb\_est59.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result	Query	Match	Length	DB	ID	Description
c 1	420.8	68.0	588	39	CB6502	CB6502 CB6502 Mous
c 2	190.4	30.8	576	30	AA206019	AA206019 zq5406.s

C	3	175..8	28..4	431	63	A1978828	MF6004..x
C	4	159..8	361	30	AA231372		
C	5	119..6	348	69	AA139620	UT-R-821..	
C	6	119..6	323..0	105	AF090533	9996611..x	
C	7	110..4	380	74	AF024023		
C	8	118..19..1	291	28	AA077918	7811805..x	
C	9	118..19..1	221	28	AA077918	7811805..x	
C	10	176..8	12..4	42	AF148805		
C	11	82..4	1036	79	CSN01085		
C	12	46..7	95	997	79	CSN0057E	
C	13	42..4	68	77	CSN0091P		
C	14	42..4	68	77	CSN0091P		
C	15	42	68	77	CSN012MT		
C	16	41..8	68	386	23	H47817	
C	17	41..8	68	386	23	H47817	
C	18	41..4	67	74	79	CSN00C3A	
C	19	41..2	67	1014	79	CSN00HGX	
C	20	41..2	67	1028	80	CSN015AB	
C	21	40..0	65	101	79	CSN0062G	
C	22	40..0	65	101	79	CSN0062G	
C	23	39..8	64	588	48	A155788	
C	24	39..8	64	910	79	CSN006GN	
C	25	39..8	64	910	79	CSN006GN	
C	26	39..8	64	901	26	H28574	
C	27	39..6	64	901	26	H28574	
C	28	39..6	64	1101	80	CSN044PA	
C	29	39..4	63	1101	80	CSN072M	
C	30	39..4	63	1101	80	CSN072M	
C	31	39..2	63	602	79	CSN10M6	
C	32	39..2	63	779	87	A074804	
C	33	39..2	63	859	79	CSN012RD	
C	34	39..2	63	859	79	CSN012RD	
C	35	39	63	615	88	A087633	
C	36	39	63	744	80	CSN072K	
C	37	38	63	811	79	CSN0118C	
C	38	38	62	844	79	CSN0052P	
C	39	38	62	844	79	CSN0052P	
C	40	38	62	1201	80	CSN0181P	
C	41	38	62	1201	80	CSN0181P	
C	42	38	62	1059	80	CSN0155T	
C	43	38	62	1059	80	CSN0155T	
C	44	38	62	453	26	H77793	
C	45	38	62	498	79	CSN0081N	
C	46	38	62	498	79	CSN0081N	

FEATURES	Location/Qualifiers
source	11-MAR-1998
	/organism="Mus musculus"
	/db_xref="taxon:10090"
	/clone="J0227G10"
	/clone_lib="House fertilized one-cell-embryo cDNA"
	/organism="Mus musculus"
	/clone_lib="House fertilized one-cell-embryo"
	/others
BASE COUNT	145 a 134 c 193 g 112 t
ORIGIN	
Query Match	68.0%; Score 420.8; DB 39; Length 588;
Best Local Similarity	Matches 49; Conservative 0; Mismatches 26; Indels 5; Gaps 5;
QY 102 gccggtgttcaaacctcccaatcaactcaactggtctgctccctccctccctccccc	161
Db 586 gccgttt	528
QY 162 tctgtccaaagctcttcaactatgcttctgttctgctgctgctgctgctgctgctgctg	219
Db 527 ttatcccttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttctt	468
QY 220 caactgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctg	279
Db 467 atct	410
QY 280 gctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctg	339
Db 405 cact	350
QY 340 cttct	399
Db 345 cttct	290
QY 400 cttct	459
Db 385 cttct	230
QY 460 tctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctg	519
Db 225 tttct	170
QY 520 tttct	579
Db 165 tttct	110
QY 580 ctatgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctg	619
Db 105 ctatgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctg	70
RESULT 2	576 bp mRNA
AA206019/C	LOCUS
DEFINITION	Z95406.21 Stageone neuroepithelium (937231) Homo sapiens cDNA
ACCESSION	AA206019
VERSION	1
AUTHORS	EST
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
AUTHORS	Hillier, B., Aken, B., Bowles, L., Dubuque, T., Gieseler, G., Jost, S.,
	Kizama, H., Kizama, T., Lacy, M., Le, L., Lennon, G., Marra, M.,
	Matsuda, Y., Moore, S., Schellenberg, R., Stepien, K., Tan, F.,
	Wash-NCI human EST project
TITLE	On Jan 23, 1995 this sequence version replaced gi:637755.
JOURNAL	
COMMENT	

c 3	159.8	26.4	31	53	A1378828	w6c04.x
c 4	159.8	26.4	31	53	A1378828	w6c04.x
c 5	159.8	26.4	31	53	A1378828	w6c04.x
c 6	159.8	26.4	31	53	A1378828	w6c04.x
c 7	159.8	26.4	31	53	A1378828	w6c04.x
c 8	159.8	26.4	31	53	A1378828	w6c04.x
c 9	159.8	26.4	31	53	A1378828	w6c04.x
c 10	159.8	26.4	31	53	A1378828	w6c04.x
c 11	159.8	26.4	31	53	A1378828	w6c04.x
c 12	159.8	26.4	31	53	A1378828	w6c04.x
c 13	159.8	26.4	31	53	A1378828	w6c04.x
c 14	159.8	26.4	31	53	A1378828	w6c04.x
c 15	159.8	26.4	31	53	A1378828	w6c04.x
c 16	159.8	26.4	31	53	A1378828	w6c04.x
c 17	159.8	26.4	31	53	A1378828	w6c04.x
c 18	159.8	26.4	31	53	A1378828	w6c04.x
c 19	159.8	26.4	31	53	A1378828	w6c04.x
c 20	159.8	26.4	31	53	A1378828	w6c04.x
c 21	159.8	26.4	31	53	A1378828	w6c04.x
c 22	159.8	26.4	31	53	A1378828	w6c04.x
c 23	159.8	26.4	31	53	A1378828	w6c04.x
c 24	159.8	26.4	31	53	A1378828	w6c04.x
c 25	159.8	26.4	31	53	A1378828	w6c04.x
c 26	159.8	26.4	31	53	A1378828	w6c04.x
c 27	159.8	26.4	31	53	A1378828	w6c04.x
c 28	159.8	26.4	31	53	A1378828	w6c04.x
c 29	159.8	26.4	31	53	A1378828	w6c04.x
c 30	159.8	26.4	31	53	A1378828	w6c04.x
c 31	159.8	26.4	31	53	A1378828	w6c04.x
c 32	159.8	26.4	31	53	A1378828	w6c04.x
c 33	159.8	26.4	31	53	A1378828	w6c04.x
c 34	159.8	26.4	31	53	A1378828	w6c04.x
c 35	159.8	26.4	31	53	A1378828	w6c04.x
c 36	159.8	26.4	31	53	A1378828	w6c04.x
c 37	159.8	26.4	31	53	A1378828	w6c04.x
c 38	159.8	26.4	31	53	A1378828	w6c04.x
c 39	159.8	26.4	31	53	A1378828	w6c04.x
c 40	159.8	26.4	31	53	A1378828	w6c04.x
c 41	159.8	26.4	31	53	A1378828	w6c04.x
c 42	159.8	26.4	31	53	A1378828	w6c04.x
c 43	159.8	26.4	31	53	A1378828	w6c04.x
c 44	159.8	26.4	31	53	A1378828	w6c04.x
c 45	159.8	26.4	31	53	A1378828	w6c04.x

## ALIGNMENTS

RESULT 1		588 bp mRNA	
C86502/C		LOCUS	
DEFINITION		J0227G10.3' mRNA sequence.	
ACCESSION		C86502	
VERSION		1	
AUTHORS		EST	
ORGANISM		Mus musculus	
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;	
AUTHORS		Hillier, B., Aken, B., Bowles, L., Dubuque, T., Gieseler, G., Jost, S.,	
TITLE		Kizama, H., Kizama, T., Lacy, M., Le, L., Lennon, G., Marra, M.,	
JOURNAL		Matsuda, Y., Moore, S., Schellenberg, R., Stepien, K., Tan, F.,	
COMMENT		Wash-NCI human EST project	
		On Jan 23, 1995 this sequence version replaced gi:1407150.	

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OM nucleic - nucleic search, using sv model

Run on:

March 24, 2000, 10:42:11 ; Search time 5166.57 seconds  
(without alignments)  
-843.347 Million cell updates/sec

Title: US-09-276-268-6

Perfect score: 1435

Sequence:

Scoring table: 1 CAGGGCGCTGCTGCG.....CAGCGTAAGCACTG 1435

IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 821193 seqs. -1518197014 residues

Total number of hits satisfying chosen parameters: 164286

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

1: GenBank1.\*

2: gb\_hum1.\*

3: gb\_hum2.\*

4: gb\_hum3.\*

5: gb\_ov.\*

6: gb\_ph.\*

7: gb\_p1.\*

8: gb\_p2.\*

9: gb\_p3.\*

10: gb\_p4.\*

11: gb\_p5.\*

12: gb\_p6.\*

13: gb\_p7.\*

14: gb\_p8.\*

15: gb\_p9.\*

16: gb\_p10.\*

17: gb\_p11.\*

18: gb\_hum1.\*

19: gb\_hum2.\*

20: gb\_hum3.\*

21: gb\_ov.\*

22: gb\_ph.\*

23: gb\_p1.\*

24: gb\_p2.\*

25: gb\_p3.\*

26: gb\_p4.\*

27: gb\_p5.\*

28: gb\_p6.\*

29: gb\_p7.\*

30: gb\_p8.\*

31: gb\_p9.\*

32: gb\_p10.\*

33: gb\_hum1.\*

34: gb\_hum2.\*

35: gb\_hum3.\*

36: gb\_ov.\*

37: gb\_ph.\*

38: gb\_p1.\*

39: gb\_p2.\*

40: gb\_p3.\*

41: gb\_p4.\*

42: gb\_p5.\*

43: gb\_p6.\*

44: gb\_p7.\*

45: gb\_p8.\*

Pred. No. is the number of results predicted by chance to have a  
score equal to or greater than the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result	No.	Score	Query Match	Length	DB ID	Description
1	45	532.6	30.0	113497	10	AF062334 Homo sapi
2	439.8	30.0	113497	10	AC006234	AC006234 Homo sapi
3	12	9.9	339	13	G37764	G37764 Saccaromy
4	2	5.0	7218	5	166494	166494 Sequence 14
5	2	5.0	7218	5	166494	166494 Sequence 14
6	45.8	3.2	13281	34	AF043149	AC002327 Mus muscu
7	45.3	3.1	96106	45	AC017015	AC017015 Homo sapi
8	42.4	3.0	150029	41	AC009447	AC009447 Homo sapi
9	42.4	3.0	150029	41	AC009447	AC009447 Homo sapi
10	42.4	3.0	43058	9	HS0261	300184 Human alpha
11	42.2	2.9	742	40	AF000672	AF000672 Homo sapi
12	42.2	2.9	2266	9	H02663	AL035245 Drosophila
13	42.2	2.9	2266	9	H02663	AL035245 Drosophila
14	42.2	2.9	77656	45	AC017532	AC017532 Homo sapi
15	41.6	2.9	23306	2	AF058302	AF058302 Streptococ
16	41.6	2.9	38414	1	MT0002	AL008967 Mycobacte
17	41.6	2.9	174707	45	AC011092	AL122020 Human chr
18	41.6	2.9	232426	33	HS108622	AL122020 Human chr
19	41.6	2.9	202776	41	AC007871	AL109910 Homo sapi
20	41.6	2.9	202776	41	AC007871	AL109910 Homo sapi
21	41	2.9	100516	32	HS31713	227634 Homo sapien
22	41	2.9	100516	32	HS31713	227634 Homo sapien
23	41	2.9	107475	45	AC011106	AC011106 Homo sapi
24	40.8	2.8	2003	5	AB022412	AB022412 Sequence
25	40.8	2.8	2003	5	AB022412	AB022412 Sequence
26	40.8	2.8	5123	16	HEPVTE	AB028990 Sequence
27	40.8	2.8	8438	16	SHLUT	M57505 Pseudocric
28	40.8	2.8	28278	10	AC000402	AC000402 Genomic s
29	40.8	2.8	81463	45	AC016882	AC017302 Homo sapi
30	40.6	2.8	110000	45	AC017014.1	Continuation (2 of
31	40.6	2.8	110000	45	AC017014.1	Continuation (2 of
32	40.6	2.8	159787	35	AC017082	AC017082 Homo sapi
33	40.6	2.8	159787	35	AC017082	AC017082 Homo sapi
34	40.4	2.8	837	40	H02641	AV086515 Homo sapi
35	40.4	2.8	1548	9	HSEKX1	Y11432 H. sapiens e
36	40.4	2.8	42555	1	SC727	AL061634 Homo sapi
37	40.4	2.8	42555	1	SC727	AL061634 Homo sapi
38	40.4	2.8	156601	10	HS21265	AL009172 Streptococ
39	40.4	2.8	190000	33	AC004479	AC004479 Homo sapi
40	40.4	2.8	190000	33	AC004479	AC004479 Homo sapi
41	40.2	2.8	31636	1	SC727	Y08222 H. sapiens M
42	40.2	2.8	214258	42	AC009108	AC009108 Streptococ
43	40.2	2.8	214258	42	AC009108	AC009108 Streptococ
44	40	2.8	3397	9	HSDNATEF1	X84839 H. sapiens T
45	39.8	2.8	42310	1	SCU22	M63896 Homo sapien
						AL031124 Streptococ

## ALIGNMENTS

Result: 1  
AF062534  
LOCUS: AF062534  
DEFINITION: Homo sapiens gemethionin 1 mRNA, complete cds.  
VERSION: AF062534.1  
KEYWORDS: 2340 bp mRNA PRI 24-NOV-1998





[illegible]

2  
 RESULT :  
 : Sequence 1, Application US/08972008  
 : Patent No. 5942401  
 : GENETIC INFORMATION  
 : APPLICANT: Holzman, Douglas A.  
 : TITLE OF INVENTION: No. 5942401e1 Molecules of the Pollistatin-Related  
 : NUMBER OF SEQUENCES: 5  
 : CORRESPONDENCE ADDRESS: COCHWILL, LLP  
 : STREET: 28 State Street  
 : CITY: Boston  
 : STATE: Massachusetts  
 : COUNTRY: USA  
 : ZIP: 02109  
 : COMPUTER READABLE FORM:  
 : MEDIUM TYPE: Floppy disk  
 : COMPUTER: IBM PC compatible  
 : SOFTWARE: SYSTEM PC-008/MS-008  
 : CURRENT APPLICATION DATA: Release #1.0, Version #1.25  
 : APPLICATION NUMBER: US/08/972,008

CLASSIFICATION: 435  
AGENT INFORMATION:

RESULT  
225348-2  
Patient  
Ap. N.

NAME: JAY E. HARRINGTON  
REGISTRATION NUMBER: 207  
REFERENCE/DOCKET NUMBER: MXI-026  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)27-7400  
TELEFAX: (617)42-4214  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2325 base pairs  
TYPE: nucleic acid  
STR: none  
TOPOLOGY: single  
MOLWT: 1500000  
MOLWGT TYPE: CDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 23..814  
US-08-977-008-1

US-08-972-008-1

LOCATION: 43.814	
Query Match	43.94; Score 495.8; DB 4; Length 2525;
Best Local Similarity	81.14; Pred. No. 1.1e-125;
Matches 614; Conservative	0; Mismatches 137; Indels 6;

[illegible]











GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: March 24, 2000, 11:00:19 : Search time 3693.2 Seconds  
(without alignments)  
880,902 Million cell updates/sec

Title: US-09-276-268-9

File: score: 815

Sequence: 1 agtgcgacatgagatcc.....gtatatacaagatgac 815

Scoring table: IDENTITY\_NUC

Gapop 10.0, Gapext 1.0

Searched: 4538634 seqs, 1887831982 residues

Total number of hits satisfying chosen parameters: 9077268

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match ON

Listing first 45 summaries

Database :

EST.\*

1: em.est1.\*

2: em.est2.\*

3: em.est3.\*

4: em.est4.\*

5: em.est5.\*

6: em.est6.\*

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40: em.est40.\*

41: em.est41.\*

42: em.est42.\*

43: em.est43.\*

44: em.est44.\*

45: gb.est26.\*  
46: gb.est27.\*  
47: gb.est28.\*  
48: gb.est29.\*  
49: gb.est30.\*  
50: gb.est31.\*  
51: gb.est32.\*  
52: em.est20.\*  
53: em.est21.\*  
54: em.est22.\*  
55: em.est23.\*  
56: em.est24.\*  
57: em.est25.\*  
58: em.est26.\*  
59: gb.est33.\*  
60: gb.est34.\*  
61: gb.est35.\*  
62: gb.est36.\*  
63: gb.est37.\*  
64: gb.est38.\*  
65: gb.est39.\*  
66: em.est28.\*  
67: em.est29.\*  
68: em.est30.\*  
69: em.est31.\*  
70: em.est32.\*  
71: gb.est41.\*  
72: gb.est42.\*  
73: gb.est43.\*  
74: gb.est44.\*  
75: em.est31.\*  
76: em.est32.\*  
77: em.est33.\*  
78: em.est34.\*  
79: gb.est41.\*  
80: gb.est42.\*  
81: gb.est43.\*  
82: gb.est44.\*  
83: em.est31.\*  
84: em.est32.\*  
85: em.est33.\*  
86: em.est34.\*  
87: gb.est41.\*  
88: gb.est42.\*  
89: gb.est43.\*  
90: gb.est44.\*  
91: gb.est41.\*  
92: gb.est42.\*  
93: em.est36.\*  
94: em.est37.\*  
95: em.est38.\*  
96: em.est39.\*  
97: em.est40.\*  
98: em.est41.\*  
99: gb.est41.\*  
100: gb.est42.\*  
101: em.est42.\*  
102: gb.est42.\*  
103: gb.est43.\*  
104: gb.est44.\*  
105: gb.est45.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the best result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result	Query	No.	Score	Match	Length	DB	ID	Description
1	550.2	67.5	591	46	AI466595			AI466595 mg73412.y
2	466.8	57.3	470	44	AI287088			AI287088 U15601.y

us-09-276-268-9.rst

24 17:28:47 2000

[illegible]

GenCase version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: March 24, 2000, 11:00:01 : Search time 3493.2 Seconds  
(without alignments)  
1222.454 Million cell updates/sec

Title: us-09-276-268-7

Score: 1.99

Sequence: 1.99acacgcgcgcctctct.....aaagacactctgaagcaga 1131

Scoring table:

IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4538634 seqs, 1887831982 residues

Total number of hits satisfying chosen parameters: 9077268

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

EST.\*

1: em\_est1.\*

2: em\_est2.\*

3: em\_est3.\*

4: em\_est4.\*

5: em\_est5.\*

6: em\_est6.\*

7: em\_est7.\*

8: em\_est8.\*

9: em\_est9.\*

10: em\_est10.\*

11: em\_est11.\*

12: em\_est12.\*

13: em\_est13.\*

14: em\_est14.\*

15: em\_est15.\*

16: em\_est16.\*

17: em\_est17.\*

18: em\_est18.\*

19: em\_est19.\*

20: em\_est20.\*

21: em\_est21.\*

22: em\_est22.\*

23: em\_est23.\*

24: em\_est24.\*

25: em\_est25.\*

26: em\_est26.\*

27: em\_est27.\*

28: em\_est28.\*

29: em\_est29.\*

30: em\_est30.\*

31: em\_est31.\*

32: em\_est32.\*

33: em\_est33.\*

34: em\_est34.\*

35: em\_est35.\*

36: em\_est36.\*

37: em\_est37.\*

38: em\_est38.\*

39: em\_est39.\*

40: em\_est40.\*

41: em\_est41.\*

42: em\_est42.\*

43: em\_est43.\*

44: em\_est44.\*

45: gb\_est26.\*  
46: gb\_est27.\*  
47: gb\_est28.\*  
48: gb\_est29.\*  
49: gb\_est30.\*  
50: gb\_est31.\*  
51: gb\_est32.\*  
52: gb\_est33.\*  
53: em\_est20.\*  
54: em\_est22.\*  
55: em\_est23.\*  
56: em\_est24.\*  
57: em\_est25.\*  
58: em\_est26.\*  
59: gb\_est33.\*  
60: gb\_est34.\*  
61: gb\_est35.\*  
62: gb\_est36.\*  
63: gb\_est37.\*  
64: gb\_est38.\*  
65: gb\_est39.\*  
66: em\_est28.\*  
67: em\_est29.\*  
68: em\_est30.\*  
69: gb\_est39.\*  
70: gb\_est40.\*  
71: gb\_est41.\*  
72: gb\_est42.\*  
73: gb\_est43.\*  
74: gb\_est44.\*  
75: em\_est31.\*  
76: em\_est32.\*  
77: em\_est33.\*  
78: em\_est34.\*  
79: gb\_est41.\*  
80: gb\_est42.\*  
81: gb\_est43.\*  
82: gb\_est44.\*  
83: em\_est31.\*  
84: em\_est32.\*  
85: em\_est33.\*  
86: em\_est34.\*  
87: gb\_est45.\*  
88: gb\_est46.\*  
89: gb\_est47.\*  
90: gb\_est48.\*  
91: gb\_est49.\*  
92: em\_est35.\*  
93: em\_est36.\*  
94: em\_est37.\*  
95: em\_est38.\*  
96: em\_est39.\*  
97: em\_est40.\*  
98: em\_est41.\*  
99: gb\_est50.\*  
100: gb\_est51.\*  
101: em\_est42.\*  
102: gb\_est52.\*  
103: gb\_est53.\*  
104: gb\_est54.\*  
105: gb\_est55.\*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the best matching printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result	Score	Query	Match	Length	DB	ID	Description
1	553.8	49.0	591	41	A1050489		A1050489
2	537.8	47.6	570	28	A116725		A116725 mp24904.7





```

0000CCACCACTTGTGGAGGAGCACCAGGCGGCCGCCTTCGACTACATATAAAA 357
Qy 498 gaagctgtcccctccaa 565
Db 558 GmACGGTTTCCCCTCAA 574

RESULT 2
PARTIAL SEQUENCE
LOCUS      AALL16725       570 bp      mRNA
DEFINITION m44904.1 Barstead MRLR1 Mus musculus cDNA clone IMAGE:573702 5' similar to NP_049C12.12 CEO3372 ; mRNA sequence.
ACCESSION   AALL16725.1 GI:1671734
VERSION     AALL16725.1 GI:1671734
KEYWORDS    EST
SOURCE      Mouse house.
ORGANISM   Mus musculus.
Eukaryota; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Mar (bases to 570)
Geisel,S., Kucaba,T., Allen,M., Boyles,M., Dietrich,N., Dubique,T., Schellenberg,K., Septeom,M., Tan,F., Underwood,K., Wozniak,W., Weisinger,B., Wyler,T., Lennon,G., Soares,B., Wilson,R. and The WashU-HMNI Mouse EST Project
Unpublished (1996).
Sep 17, 1996 this sequence version replaced GI:1397422.
WashU-HMNI Mouse EST Project
Washington University School of Medicine
Tel# 314-286 Park Parkway, Box 8501, St. Louis, MO 63109.
Fax: 314 286 1810
Email: mouseest@wustl.edu
This database is available royalty free through LBL & contact the IMAGE Consortium (liftoimage.lbl.gov) for further information.
Seq primer: -2hm3 rev2 Et from Amerham
High quality sequence spot: 505.
Location/Qualifiers
1. 570
/orfsize=Mus musculus*
/cd_name=cd/c
/db_xref=tac/10090*
/cdname=IMAGE:573702
/cclone_lib=Barstead MRLR1*
/cdate=1996
/clisise_type=Kinezo*
/dev_stage=6 weeks
/db_xref=pubmed/10090
/polynucleotide=Trp-Pac (pharmacia) with a modified polynucleotide site 1 to oligo(dN) primer [5 strand cdna was primed with a Not I - oligo(dN) primer] [5 strand cdna 3'overhangATTAGTGAGGACGGCCGCGCGGTTTTTTTTTTTTTTTTTTTTCATCATGATCGTCGAC] cDNA was ligated to Eco RI adaptors (CATGATTCGTCGAC) digested with Eco RI and cloned into the Not I and Eco RI sites of the modified pMTV vector. Library constructed by Bob Barstead.*
109 a 189 c 133 g 139 t

BASE COUNT
ORIGIN
Query Match 47.6%; Score 437.8; DB 28; Length 570;
Best Local Similarity 99.9%; Pred. No. 4.7e-112; Indels 1; Gaps 1;
Y 9 ccgccttgctgctcgcactctgcagcttcctccatccctccgccctccacg 68
b 19 CCACGGCTTCCTGCTCCCGCTGATCTCCAGGATTCCTCCCTACCTCCGCCTCCAGGC 78
y 69 ctgcctcgctctggctggcgaagtctgcgcctctgcgcctctgcctcctggctggg 128

```







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OM nucleic - nucleic search, using sw model

Run on: March 24, 2000, 10:59:29 : Search time 1493.2 Seconds  
4538634 seqs, 188781982 residues  
659,053 Million cell updates/sec

Title: US-09-276-268-3  
Perfect score: 619  
Sequence: 1 ggcacaggagagccctgc.....tggcgcaagagccactta 619

Scoring table: HUGBURY-MC  
Gapop 110.0, Gapext 1.0

Searched: 4538634 seqs, 188781982 residues  
Total number of hits satisfying chosen parameters: 907268

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

EST.\*

1: em.est1.\*  
2: em.est2.\*  
3: em.est3.\*  
4: em.est4.\*  
5: em.est5.\*  
6: em.est6.\*  
7: em.est7.\*  
8: em.est8.\*  
9: em.est9.\*  
10: em.est10.\*  
11: em.est11.\*  
12: em.est12.\*  
13: em.est13.\*  
14: em.est14.\*  
15: em.est15.\*  
16: em.est16.\*  
17: em.est17.\*  
18: em.est18.\*  
19: em.est19.\*  
20: em.est20.\*  
21: em.est21.\*  
22: em.est22.\*  
23: em.est23.\*  
24: em.est24.\*  
25: em.est25.\*  
26: em.est26.\*  
27: em.est27.\*  
28: em.est28.\*  
29: em.est29.\*  
30: em.est30.\*  
31: em.est31.\*  
32: em.est32.\*  
33: em.est33.\*  
34: em.est34.\*  
35: em.est35.\*  
36: em.est36.\*  
37: em.est37.\*  
38: em.est38.\*  
39: em.est39.\*  
40: em.est40.\*  
41: em.est41.\*  
42: em.est42.\*  
43: em.est43.\*  
44: em.est44.\*  
45: em.est45.\*

43: gb.est26.\*  
44: gb.est27.\*  
45: gb.est28.\*  
46: gb.est29.\*  
47: gb.est30.\*  
48: gb.est31.\*  
49: gb.est32.\*  
50: gb.est33.\*  
51: gb.est34.\*  
52: gb.est35.\*  
53: em.est21.\*  
54: em.est22.\*  
55: em.est23.\*  
56: em.est24.\*  
57: em.est25.\*  
58: em.est26.\*  
59: gb.est33.\*  
60: gb.est34.\*  
61: gb.est35.\*  
62: gb.est36.\*  
63: gb.est37.\*  
64: gb.est38.\*  
65: em.est26.\*  
66: em.est27.\*  
67: em.est28.\*  
68: em.est30.\*  
69: em.est31.\*  
70: gb.est40.\*  
71: gb.est41.\*  
72: gb.est42.\*  
73: gb.est43.\*  
74: gb.est44.\*  
75: em.est41.\*  
76: em.est42.\*  
77: em.est43.\*  
78: em.est44.\*  
79: gb.est41.\*  
80: gb.est42.\*  
81: gb.est43.\*  
82: gb.est44.\*  
83: em.est41.\*  
84: em.est42.\*  
85: em.est43.\*  
86: em.est44.\*  
87: gb.est43.\*  
88: gb.est44.\*  
89: gb.est45.\*  
90: gb.est46.\*  
91: gb.est47.\*  
92: em.est45.\*  
93: em.est46.\*  
94: em.est47.\*  
95: em.est48.\*  
96: em.est49.\*  
97: em.est50.\*  
98: em.est51.\*  
99: gb.est50.\*  
100: gb.est51.\*  
101: em.est51.\*  
102: gb.est51.\*  
103: gb.est51.\*  
104: gb.est51.\*  
105: gb.est51.\*

Pred. NO. is the number of results predicted by chance to have a  
score at least as high as the observed score, assuming random  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result

Query

Match Length DB ID

Description

C 1 420.8 58.0 58.0 30 584502  
C 2 190.4 30.8 30.8 30 44308019

584502  
44308019 2544009.3

FEATURES	Source	Location/Qualifiers
AS178828 wtC004.X		
3 175.8 28.8	431 63	AS178828 wtC004.X
4 159.8 35.4	361 30	AA231372 wt0008.X
5 141.6 22.9	380 43	AA139620 UI-B-B11.X
6 131.6 22.9	380 43	AA139620 UI-B-B11.X
7 130.4 21.1	380 74	AA204025 G354ell1.X
8 118.8 19.1	251 28	AA077918 YH1805.C
9 118.8 19.1	251 28	AA077918 YH1805.C
10 118.8 19.1	251 28	AA077918 YH1805.C
11 118.8 19.1	251 28	AA077918 YH1805.C
12 118.8 19.1	251 28	AA077918 YH1805.C
13 118.8 19.1	251 28	AA077918 YH1805.C
14 118.8 19.1	251 28	AA077918 YH1805.C
15 118.8 19.1	251 28	AA077918 YH1805.C
16 118.8 19.1	251 28	AA077918 YH1805.C
17 118.8 19.1	251 28	AA077918 YH1805.C
18 118.8 19.1	251 28	AA077918 YH1805.C
19 118.8 19.1	251 28	AA077918 YH1805.C
20 118.8 19.1	251 28	AA077918 YH1805.C
21 118.8 19.1	251 28	AA077918 YH1805.C
22 118.8 19.1	251 28	AA077918 YH1805.C
23 118.8 19.1	251 28	AA077918 YH1805.C
24 118.8 19.1	251 28	AA077918 YH1805.C
25 118.8 19.1	251 28	AA077918 YH1805.C
26 118.8 19.1	251 28	AA077918 YH1805.C
27 118.8 19.1	251 28	AA077918 YH1805.C
28 118.8 19.1	251 28	AA077918 YH1805.C
29 118.8 19.1	251 28	AA077918 YH1805.C
30 118.8 19.1	251 28	AA077918 YH1805.C
31 118.8 19.1	251 28	AA077918 YH1805.C
32 118.8 19.1	251 28	AA077918 YH1805.C
33 118.8 19.1	251 28	AA077918 YH1805.C
34 118.8 19.1	251 28	AA077918 YH1805.C
35 118.8 19.1	251 28	AA077918 YH1805.C
36 118.8 19.1	251 28	AA077918 YH1805.C
37 118.8 19.1	251 28	AA077918 YH1805.C
38 118.8 19.1	251 28	AA077918 YH1805.C
39 118.8 19.1	251 28	AA077918 YH1805.C
40 118.8 19.1	251 28	AA077918 YH1805.C
41 118.8 19.1	251 28	AA077918 YH1805.C
42 118.8 19.1	251 28	AA077918 YH1805.C
43 118.8 19.1	251 28	AA077918 YH1805.C
44 118.8 19.1	251 28	AA077918 YH1805.C
45 118.8 19.1	251 28	AA077918 YH1805.C

Contract:  
No.

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OM nucleic - nucleic search, using sw model

Run on: March 24, 2000, 10:59:23 : Search time 3493.2 seconds

(without alignments)

744713 Million cell updates/rec

Title: US-09-276-268-2

Raw data score:

Sequences: 1 stgcctcaggtccgcgcg,.....tgatccctcagctctctg 689

Scoring table:

Gapop 10.0 , Gapext 1.0

Searched: 4538634 seqs, 188781982 residues

Total number of hits satisfying chosen parameters: 907266

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

EST:

1: em\_est1.\*

2: em\_est2.\*

3: em\_est3.\*

4: em\_est4.\*

5: em\_est5.\*

6: em\_est6.\*

7: em\_est7.\*

8: em\_est8.\*

9: em\_est9.\*

10: em\_est10.\*

11: em\_est11.\*

12: em\_est12.\*

13: em\_est13.\*

14: em\_est14.\*

15: em\_est15.\*

16: em\_est16.\*

17: em\_est17.\*

18: em\_est18.\*

19: em\_est19.\*

20: em\_est20.\*

21: em\_est21.\*

22: em\_est22.\*

23: em\_est23.\*

24: em\_est24.\*

25: em\_est25.\*

26: em\_est26.\*

27: em\_est27.\*

28: em\_est28.\*

29: em\_est29.\*

30: em\_est30.\*

31: em\_est31.\*

32: em\_est32.\*

33: em\_est33.\*

34: em\_est34.\*

35: em\_est35.\*

36: em\_est36.\*

37: em\_est37.\*

38: em\_est38.\*

39: em\_est39.\*

40: em\_est40.\*

41: em\_est41.\*

42: em\_est42.\*

43: em\_est43.\*

44: em\_est44.\*

45: gb\_est26.\*  
46: gb\_est27.\*  
47: gb\_est28.\*  
48: gb\_est29.\*  
49: gb\_est30.\*  
50: gb\_est31.\*  
51: gb\_est32.\*  
52: em\_est20.\*  
53: em\_est21.\*  
54: em\_est22.\*  
55: em\_est23.\*  
56: em\_est24.\*  
57: em\_est25.\*  
58: em\_est26.\*  
59: gb\_est33.\*  
60: gb\_est34.\*  
61: gb\_est35.\*  
62: gb\_est36.\*  
63: gb\_est37.\*  
64: gb\_est38.\*  
65: em\_est27.\*  
66: em\_est28.\*  
67: em\_est29.\*  
68: em\_est30.\*  
69: gb\_est39.\*  
70: gb\_est40.\*  
71: gb\_est41.\*  
72: gb\_est42.\*  
73: gb\_est43.\*  
74: gb\_est44.\*  
75: em\_est31.\*  
76: em\_est32.\*  
77: em\_est33.\*  
78: em\_est34.\*  
79: gb\_est45.\*  
80: gb\_est46.\*  
81: gb\_est47.\*  
82: gb\_est48.\*  
83: em\_est35.\*  
84: em\_est36.\*  
85: em\_est37.\*  
86: gb\_est49.\*  
87: gb\_est50.\*  
88: gb\_est51.\*  
89: gb\_est52.\*  
90: gb\_est53.\*  
91: gb\_est54.\*  
92: em\_est39.\*  
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94: em\_est41.\*  
95: em\_est42.\*  
96: em\_est43.\*  
97: em\_est44.\*  
98: em\_est45.\*  
99: gb\_est55.\*  
100: gb\_est56.\*  
101: gb\_est57.\*  
102: gb\_est58.\*  
103: gb\_est59.\*  
104: gb\_est60.\*  
105: gb\_est61.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
2	256	80.7	560	60	AI19688
					AI19688 u0504.y
					AI19688 u42906.y











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OM nucleic - nucleic search, using sw model

Run on: March 24, 2000, 08:22:03 : Search time 3493.2 seconds  
(without alignments)  
867.931 Million cell updates/sec

Title: US-09-276-268-1  
Perfect score: 803  
Sequence: 1 gttctgaatggggatag.....aaacgacattctgagatt 803

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4538634 seqs, 188781982 residues

Total number of hits satisfying chosen parameters: 9077268

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Watch 0s  
Listing first 45 summaries

Database :

EST	est1	est2	est3	est4	est5	est6	est7	est8	est9	est10	est11	est12	est13	est14	est15	est16	est17	est18	est19	est20	est21	est22	est23	est24	est25	est26	est27	est28	est29	est30	est31	est32	est33	est34	est35	est36	est37	est38	est39	est40	est41	est42	est43	est44	est45
1	em_est1	em_est2	em_est3	em_est4	em_est5	em_est6	em_est7	em_est8	em_est9	em_est10	em_est11	em_est12	em_est13	em_est14	em_est15	em_est16	em_est17	em_est18	em_est19	em_est20	em_est21	em_est22	em_est23	em_est24	em_est25	em_est26	em_est27	em_est28	em_est29	em_est30	em_est31	em_est32	em_est33	em_est34	em_est35	em_est36	em_est37	em_est38	em_est39	em_est40	em_est41	em_est42	em_est43	em_est44	em_est45

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result	Query	Score	Match	Length	DB	ID	Description
c 1	560.6	69.8	588	69	AM107659	AM107659 um22e08.x	
2	420.8	52.4	457	36	AM646983	AM646983 vet5a06.r	

Oy	777 attattaaacgcatcttcgaagat	803
Dd	48 ATTATTAAACGCATCTCTGAGAA	22

  

RESULT 2		
AB645983	457 bp	mRNA
DEFINITION	v645983.r1 Soay disease virus gland NIDMG Mus musculus cDNA clone	
KEYWORDS	DEFINITION	
ABSTRACT		
REFERENCES		
COMMENTS		
FEATURES		
ORIGIN		
BASES		
DATE		
ANALYST		
LABORATORY		
PROJECT		
PI		
COLLEGE		
UNIVERSITY		
COUNTRY		
STATE		
CITY		
ZIP		
TELEPHONE		
FAX		
E-MAIL		
WWW		
FTP		
LOCAL		
REMOTE		
ARCHIVE		
INDEXED		
SERIALIZED		
FILED		
ENTRY		
RECORD		
STATUS		
REMARKS		
NOTES		
DESCRIPTION		
SEQUENCE		
ANNOTATION		
EDITING		
FORMATTING		
PRINTING		
STORAGE		
RETRIEVAL		
DISSEMINATION		
PROTECTION		
REGISTRATION		
PUBLICATION		
DEPOSITION		
ACCUMULATION		
MANAGEMENT		
Maintenance		
Update		
Revision		
Version		
Release		
Accession		
Submission		
Receipt		
Check		
Verify		
Confirm		
Validate		
Authenticate		
Authorize		
Accept		
Approve		
Endorse		
Sanction		
Concur		
Consent		
Assent		
Agree		
Assure		
Guarantee		
Vouch		
Warrant		
Testify		
Attest		
Substantiate		
Corroborate		
Reinforce		
Strengthen		
Support		
Uphold		
Sustain		
Maintain		
Keep		
Hold		
Retain		
Preserve		
Protect		
Defend		
Guard		
Watch		
Observe		
Monitor		
Survey		
Inspect		
Examine		
Investigate		
Research		
Study		
Analyze		
Interpret		
Understand		
Comprehend		
Grasp		
Perceive		
Recognize		
Identify		
Distinguish		
Discriminate		
Separate		
Divide		
Partition		
Segment		
Fragment		
Breakdown		
Decompose		
Dissolve		
Melt		
Liquidate		
Annihilate		
Destroy		
Demolish		
Raze		
Level		
Flatten		
Smooth		
Polish		
Gild		
Decorate		
Adorn		
Embellish		
Ornament		
Enrich		
Enhance		
Improve		
Better		
Upgrade		
Advance		
Progress		
Develop		
Grow		
Increase		
Expand		
Enlarge		
Magnify		
Amplify		
Boost		
Elevate		
Ascend		
Rise		
Soar		
Leap		
Jump		
Hop		
Bound		

RESULT	2
AA646983	
LOCUS	AA646983 457 bp mRNA
DEFINITION	vfa3abg.r1 Soares mouse mammary gland NDMC Mus musculus cDNA clone
ACCESSION	IMAGE:21074 5', mRNA sequence.
VERSION	AA646983.1 GI:2573412

Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Mammalia:  
Eutheria: Rodentia: Sciurognathi: Muridae: Murinae: Mus.  
1 (bases 1 to 457)

REFERENCE

AUTHORS

Marta, M., Hillier, B., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,  
Geisels, S., Kucenas, T., Lacy, M., Le, M., Martin, J., Morris, M.,  
Schaltenberg, K., Seipton, K., Tan, F., Underwood, K., Moore, B.,  
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and

**TITLE** The WashU-HIMI Mouse EST Project  
**JOURNAL** Unpublished (1996)  
**COMMENT** On Sep 12, 1996 this sequence version replaced g1:1407346.  
Contact: Marra M/Mouse EST Project  
WashU-HIMI Mouse EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 9501, St. Louis, MO 63108

Email: [mousseestatson.wustl.edu](mailto:mousseestatson.wustl.edu)  
This clone is available royalty-free through LLNL; contact the  
IMAGES Consortium ([info@image.llnl.gov](mailto:info@image.llnl.gov)) for further information.  
MGI:489354  
Seq primer: -28ml3 rev2 ET from Amersham

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FEATURES
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/strain="C57BL/6J"
/ab.xref="taxon:10090"
/clone="IMAGE:821074"
/tissue="mammary gland"
/tissue.type="mammary gland"

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[illegible]

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Query Match 52.4% Score 420.8 DB 36; Length 457;  
 Best Local Similarity 98.9% Pred. No. 7.5e-113;  
 Matches 455; Conservative  
 0: Mismatches 2: Indels 3: Cases

79 ggctctcggcgctcgagagatggactctctcgcgcttgggaatctcgggcgcttgatctg 138  
|||||  
1 ggttcggcgctcgagagatggactctctcgcgcttgggaatctcgggcgcttgatctg 60

[illegible]

RESULT 3  
AI505719/C

LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

## REFERENCE

AUTHORS  
TITLE  
JOURNAL

COMPLEMENT

## FEATURES

**source**